



REPLACEMENT SHEET

Figure 20A

Alignment Report: hETBRL2p (SEQ ID NO:18) and hGRP37p (SEQ ID NO:10)

		M R A L G A L A A S L A V L L A V G L L K V S G G A A L G V G P A S R N E T C L	Majority
		10 20 30 40	
1	MRWLWPLAVSLAVILAVGLSRVSGGAPLHLG-----	hETBRL2p	
1	MRA PGAL LARMSRL L L L L L L K V S A S S A L G V A P A S R N E T C L	hGRP37p	
		G E S C A P T V I O R R G R D A W G P G N S A R D V L R A R A E T E E Q G A A F	Majority
		50 60 70 80	
32	-----R H R A E T Q E Q Q S - -	hETBRL2p	
41	G E S C A P T V I O R R G R D A W G P G N S A R D V L R A R A P R E E Q G A A F	hGRP37p	
		L A G P S W D L P A A P G R D P A A G R G A E A S A A G P P G P P T R P P G P W	Majority
		90 100 110 120	
43	-----	hETBRL2p	
81	L A G P S W D L P A A P G R D P A A G R G A E A S A A G P P G P P T R P P G P W	hGRP37p	
		R W K G A R G T E P S E T L G R G N P T A L Q L F L O I S D E E A K G V Q G A G	Majority
		130 140 150 160	
43	- - R S K R G T E - - - - - D E E A K G V Q - - -	hETBRL2p	
121	R W K G A R G Q E P S E T L G R G N P T A L Q L F L O I S E E E E K G P R G A G	hGRP37p	
		I S G R S Q E Q S V Q T V P G A S A L F Y R P I H A G G L Q G S H H K P L V A T	Majority
		170 180 190 200	
58	- - - - - Q Y V P E E W A E Y P R P I H P A G L Q P T - - K P L V A T	hETBRL2p	
161	I S G R S Q E Q S V K T V P G A S D L F Y W P R R A G K L O G S H H K P L S K T	hGRP37p	
		A N G L A G D G G W T I A L P G S G L A L N G S L G G G I H E P G G P R R G N S	Majority
		210 220 230 240	
86	S P N P D K D G G - - - - T P D S G Q E L R G N L T G A - - - P G - - - - -	hETBRL2p	
201	A N G L A G H E G W T I A L P G R A L A Q N G S L G E G I H E P G G P R R G N S	hGRP37p	
		T N Q R V Q L Q N P L Y P V T E S S Y G A Y A V M L L A V V V F G V G I V G N L	Majority
		250 260 270 280	
112	- - Q R L Q I Q N P L Y P V T E S S Y S A Y A I M L L A L V V F A V G I V G N L	hETBRL2p	
241	T N R R V R L K N P F Y P L T Q E S Y G A Y A V M C L S V V I F G T G I I G N L	hGRP37p	
		A V M C I V W H S Y Y L K S A S N S L L A S L A L W D F L V L F F C L P L V I F	Majority
		290 300 310 320	
150	S V M C I V W H S Y Y L K S A W N S I L A S L A L W D F L V L F F C L P I V I F	hETBRL2p	
281	A V M C I V C H N Y Y M R S I S N S L L A N L A F W D F L I I F F C L P L V I F	hGRP37p	
		N E L T K Q R L L G D V S C K A V P F I E V A S L G V T T F S L C A L G I D R F	Majority
		330 340 350 360	
190	N E I T K O R L L G D V S C R A V P F M E V S S L G V T T F S L C A L G I D R F	hETBRL2p	
321	H E L T K K W L L E D F S C K I V P Y I E V A S L G V T T F T L C A L C I D R F	hGRP37p	



REPLACEMENT SHEET

Figure 20B

Alignment Report: hETBRL2p (SEQ ID NO:18) and hGRP37p (SEQ ID NO:10)

H A A T S V L M K V E M I E N C S S I L A K L A V I W V G A L L L A V P E V V L																														Majority													
370 380 390 400																																											
230	H	V	A	T	S	T	L	P	K	V	R	P	I	E	R	C	Q	S	I	L	A	K	L	A	V	I	W	V	G	S	M	T	L	A	V	P	E	L	L	L		HETBRLP2p	
361	R	A	A	T	N	V	Q	M	Y	Y	E	M	I	E	N	C	S	S	T	T	A	K	L	A	V	I	W	V	G	A	L	L	L	A	L	P	E	V	V	L		HGPR37p	
R Q L A Q E D A G F S G R G T A D S C I I K I S A S L P D S L Y V L A L T Y D S																														Majority													
410 420 430 440																																											
270	W	Q	L	A	O	E	P	A	-	-	P	T	M	G	T	L	D	S	C	I	M	K	P	S	A	S	L	P	E	S	L	Y	S	L	V	M	T	Y	Q	N		HETBRLP2p	
401	R	Q	L	S	K	E	D	L	G	F	S	G	R	A	P	A	E	R	C	I	I	K	I	S	P	D	L	P	D	T	I	Y	V	L	A	L	T	Y	D	S		HGPR37p	
A R L W W Y F G C Y F C L P I L F T V T C S L V T A R K V R G A P G R E S A C T																														Majority													
450 460 470 480																																											
308	A	R	M	W	W	Y	F	G	C	Y	F	C	L	P	I	L	F	T	V	T	C	Q	L	V	T	-	W	R	V	R	G	P	P	G	R	K	S	E	C	-		HETBRLP2p	
441	A	R	L	W	W	Y	F	G	C	Y	F	C	L	P	T	L	F	T	I	T	C	S	L	V	T	A	R	K	I	R	K	A	-	-	-	E	K	A	C	T		HGPR37p	
R G S K H E I Q L E S Q L N S T V V G L T V V Y G F C I L P E N V C N I V V A Y																														Majority													
490 500 510 520																																											
346	R	A	S	K	H	E	-	Q	C	E	S	Q	L	N	S	T	V	V	G	L	T	V	V	Y	A	F	C	T	L	P	E	N	V	C	N	I	V	V	A	Y		HETBRLP2p	
478	R	G	N	K	R	Q	I	O	L	E	S	Q	M	N	C	T	V	V	A	L	T	I	L	Y	G	F	C	I	I	P	E	N	I	C	N	I	V	T	A	Y		HGPR37p	
L A T G V S Q Q T L D L L G L I S Q F L L F F K G A V T P V L L L C L C K P L G																														Majority													
530 540 550 560																																											
385	L	S	T	E	L	T	R	Q	T	L	D	L	L	G	L	I	N	Q	F	S	T	F	F	K	G	A	I	T	P	V	L	L	L	C	I	C	R	P	L	G		HETBRLP2p	
518	M	A	T	G	V	S	Q	O	T	M	D	L	L	N	I	I	S	O	F	L	L	F	F	K	S	C	V	T	P	V	L	L	F	C	L	C	K	P	F	S		HGPR37p	
Q A F L D C C C C C C C E E C G G A S S A V A A D G S D N E L T T E V S L S I F																														Majority													
570 580 590 600																																											
425	Q	A	F	L	D	C	C	C	C	C	C	C	C	E	E	C	G	G	A	S	E	A	S	A	A	N	G	S	D	N	K	L	K	T	E	V	S	S	S	I	Y		HETBRLP2p
558	R	A	F	M	E	C	C	C	C	C	C	-	E	E	C	I	Q	K	S	S	T	V	T	S	D	D	N	D	N	E	Y	T	T	E	L	E	L	S	P	F		HGPR37p	
S T I R R E S S T L A S V G T H C																														Majority													
610																																											
465	F	H	K	P	R	E	S	P	P	L	L	P	L	G	T	P	C													HETBRLP2p													
597	S	T	I	R	R	E	M	S	T	F	A	S	V	G	T	H	C													HGPR37p													

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Decoration 'Decoration #2': Box residues that match the Consensus exactly.